

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/700, 3/3A

Source: 1FW16

Date Processed by STIC: 3/21/06

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 03/21/2006

PATENT APPLICATION: US/10/700,313A

TIME: 08:49:52

Input Set : A:\seq listing.app

Output Set: N:\CRF4\03212006\J700313A.raw

3 <110> APPLICANT: Combadiere et al.
 5 <120> TITLE OF INVENTION: CC CHEMOKINE RECEPTOR 5 DNA, NEW ANIMAL MODELS AND
 THERAPEUTIC

6 AGENTS FOR HIV INFECTION

8 <130> FILE REFERENCE: 66645-01

10 <140> CURRENT APPLICATION NUMBER: US 10/700,313A

11 <141> CURRENT FILING DATE: 2003-10-31

13 <150> PRIOR APPLICATION NUMBER: US 60/018,508

14 <151> PRIOR FILING DATE: 1996-05-28

16 <150> PRIOR APPLICATION NUMBER: 08/864,458

17 <151> PRIOR FILING DATE: 1997-05-28

19 <160> NUMBER OF SEQ ID NOS: 10

21 <170> SOFTWARE: PatentIn version 3.3

23 <210> SEQ ID NO: 1

24 <211> LENGTH: 1225

25 <212> TYPE: DNA

26 <213> ORGANISM: Homo sapiens

29 <220> FEATURE:

30 <221> NAME/KEY: CDS

31 <222> LOCATION: (27)..(1082)

33 <400> SEQUENCE: 1

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35 Met Asp Tyr Gln Val Ser Ser Pro Ile

36 1 5

38 tat gac atc aat tat tat aca tcg gag ccc tgc caa aaa atc aat gtg 101

39 Tyr Asp Ile Asn Tyr Tyr Thr Ser Glu Pro Cys Gln Lys Ile Asn Val

40 10 15 20 25

42 aag caa atc gca gcc cgc ctc ctg cct ccg ctc tac tca ctg gtg ttc 149

43 Lys Gln Ile Ala Ala Arg Leu Leu Pro Pro Leu Tyr Ser Leu Val Phe

44 30 35 40

46 atc ttt ggt ttt gtg ggc aac atg ctg gtc atc ctc atc ctg ata aac 197

47 Ile Phe Gly Phe Val Gly Asn Met Leu Val Ile Leu Ile Leu Ile Asn

48 45 50 55

50 tgc aaa agg ctg aag agc atg act gac atc tac ctg ctc aac ctg gcc 245

51 Cys Lys Arg Leu Lys Ser Met Thr Asp Ile Tyr Leu Leu Asn Leu Ala

52 60 65 70

54 atc tct gac ctg ttt ttc ctt ctt act gtc ccc ttc tgg gct cac tac 293

55 Ile Ser Asp Leu Phe Phe Leu Leu Thr Val Pro Phe Trp Ala His Tyr

56 75 80 85

58 ttg gcc gcc cag tgg gac ttt gga aat aca atg tgt caa ctc ttg aca 341

59 Leu Ala Ala Gln Trp Asp Phe Gly Asn Thr Met Cys Gln Leu Leu Thr

60 90 95 100 105

62 ggg ctc tat ttt ata ggc ttc ttc tct gga atc ttc ttc atc atc ctc 389

63 Gly Leu Tyr Phe Ile Gly Phe Phe Ser Gly Ile Phe Phe Ile Ile Leu

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Input Set : A:\seq_listing.app

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66 ctg aca atc gat agg tac ctg gct gtc gtc cat gct gtg ttt gct tta 437
67 Leu Thr Ile Asp Arg Tyr Leu Ala Val Val His Ala Val Phe Ala Leu
68          125          130          135
70 aaa gcc agg acg gtc acc ttt ggg gtg gtg aca agt gtg atc act tgg 485
71 Lys Ala Arg Thr Val Thr Phe Gly Val Val Thr Ser Val Ile Thr Trp
72          140          145          150
74 gtg gtg gct gtg ttt gcg tct ctc cca gga atc atc ttt acc aga tct 533
75 Val Val Ala Val Phe Ala Ser Leu Pro Gly Ile Ile Phe Thr Arg Ser
76          155          160          165
78 caa aaa gaa ggt ctt cat tac acc tgc agc tct cat ttt cca tac agt 581
79 Gln Lys Glu Gly Leu His Tyr Thr Cys Ser Ser His Phe Pro Tyr Ser
80 170          175          180          185
82 cag tat caa ttc tgg aag aat ttc cag aca tta aag ata gtc atc ttg 629
83 Gln Tyr Gln Phe Trp Lys Asn Phe Gln Thr Leu Lys Ile Val Ile Leu
84          190          195          200
86 ggg ctg gtc ctg ccg ctg ctt gtc atg gtc atc tgc tac tcg gga atc 677
87 Gly Leu Val Leu Pro Leu Leu Val Met Val Ile Cys Tyr Ser Gly Ile
88          205          210          215
90 cta aaa act ctg ctt cgg tgt cga aat gag aag aag agg cac agg gct 725
91 Leu Lys Thr Leu Leu Arg Cys Arg Asn Glu Lys Lys Arg His Arg Ala
92          220          225          230
94 gtg agg ctt atc ttc acc atc atg att gtt tat ttt ctc ttc tgg gct 773
95 Val Arg Leu Ile Phe Thr Ile Met Ile Val Tyr Phe Leu Phe Trp Ala
96          235          240          245
98 ccc tac aac att gtc ctt ctc ctg aac acc ttc cag gaa ttc ttt ggc 821
99 Pro Tyr Asn Ile Val Leu Leu Leu Asn Thr Phe Gln Glu Phe Phe Gly
100 250          255          260          265
102 ctg aat aat tgc agt agc tct aac agg ttg gac caa gct atg cag gtg 869
103 Leu Asn Asn Cys Ser Ser Ser Asn Arg Leu Asp Gln Ala Met Gln Val
104          270          275          280
106 aca gag act ctt ggg atg acg cac tgc tgc atc aac ccc atc atc tat 917
107 Thr Glu Thr Leu Gly Met Thr His Cys Cys Ile Asn Pro Ile Ile Tyr
108          285          290          295
110 gcc ttt gtc ggg gag aag ttc aga aac tac ctc tta gtc ttc ttc caa 965
111 Ala Phe Val Gly Glu Lys Phe Arg Asn Tyr Leu Leu Val Phe Phe Gln
112          300          305          310
114 aag cac att gcc aaa cgc ttc tgc aaa tgc tgt tct att ttc cag caa 1013
115 Lys His Ile Ala Lys Arg Phe Cys Lys Cys Cys Ser Ile Phe Gln Gln
116          315          320          325
118 gag gct ccc gag cga gca agc tca gtt tac acc cga tcc act ggg gag 1061
119 Glu Ala Pro Glu Arg Ala Ser Ser Val Tyr Thr Arg Ser Thr Gly Glu
120 330          335          340          345
122 cag gaa ata tct gtg ggc ttg tgacacggac tcaagtgggc tgggtgacca 1112
123 Gln Glu Ile Ser Val Gly Leu
124          350
126 gtcagagttg tgcacatggc ttagtttttca tacacagcct gggctggggg tggggtggga 1172
128 gaggtctttt ttaaaaggaa gttactgtta tagaggggtct aagattcatc cat 1225
131 <210> SEQ ID NO: 2

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Input Set : A:\seq listing.app

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132 <211> LENGTH: 352
133 <212> TYPE: PRT
134 <213> ORGANISM: Homo sapiens
136 <400> SEQUENCE: 2
138 Met Asp Tyr Gln Val Ser Ser Pro Ile Tyr Asp Ile Asn Tyr Tyr Thr
139 1 5 10 15
142 Ser Glu Pro Cys Gln Lys Ile Asn Val Lys Gln Ile Ala Ala Arg Leu
143 20 25 30
146 Leu Pro Pro Leu Tyr Ser Leu Val Phe Ile Phe Gly Phe Val Gly Asn
147 35 40 45
150 Met Leu Val Ile Leu Ile Leu Ile Asn Cys Lys Arg Leu Lys Ser Met
151 50 55 60
154 Thr Asp Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp Leu Phe Phe Leu
155 65 70 75 80
158 Leu Thr Val Pro Phe Trp Ala His Tyr Leu Ala Ala Gln Trp Asp Phe
159 85 90 95
162 Gly Asn Thr Met Cys Gln Leu Leu Thr Gly Leu Tyr Phe Ile Gly Phe
163 100 105 110
166 Phe Ser Gly Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu
167 115 120 125
170 Ala Val Val His Ala Val Phe Ala Leu Lys Ala Arg Thr Val Thr Phe
171 130 135 140
174 Gly Val Val Thr Ser Val Ile Thr Trp Val Val Ala Val Phe Ala Ser
175 145 150 155 160
178 Leu Pro Gly Ile Ile Phe Thr Arg Ser Gln Lys Glu Gly Leu His Tyr
179 165 170 175
182 Thr Cys Ser Ser His Phe Pro Tyr Ser Gln Tyr Gln Phe Trp Lys Asn
183 180 185 190
186 Phe Gln Thr Leu Lys Ile Val Ile Leu Gly Leu Val Leu Pro Leu Leu
187 195 200 205
190 Val Met Val Ile Cys Tyr Ser Gly Ile Leu Lys Thr Leu Leu Arg Cys
191 210 215 220
194 Arg Asn Glu Lys Lys Arg His Arg Ala Val Arg Leu Ile Phe Thr Ile
195 225 230 235 240
198 Met Ile Val Tyr Phe Leu Phe Trp Ala Pro Tyr Asn Ile Val Leu Leu
199 245 250 255
202 Leu Asn Thr Phe Gln Glu Phe Phe Gly Leu Asn Asn Cys Ser Ser Ser
203 260 265 270
206 Asn Arg Leu Asp Gln Ala Met Gln Val Thr Glu Thr Leu Gly Met Thr
207 275 280 285
210 His Cys Cys Ile Asn Pro Ile Ile Tyr Ala Phe Val Gly Glu Lys Phe
211 290 295 300
214 Arg Asn Tyr Leu Leu Val Phe Phe Gln Lys His Ile Ala Lys Arg Phe
215 305 310 315 320
218 Cys Lys Cys Cys Ser Ile Phe Gln Gln Glu Ala Pro Glu Arg Ala Ser
219 325 330 335
222 Ser Val Tyr Thr Arg Ser Thr Gly Glu Gln Glu Ile Ser Val Gly Leu
223 340 345 350
226 <210> SEQ ID NO: 3

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RAW SEQUENCE LISTING

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Input Set : A:\seq listing.app

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227 <211> LENGTH: 1225
228 <212> TYPE: DNA
229 <213> ORGANISM: Homo sapiens
232 <220> FEATURE:
233 <221> NAME/KEY: CDS
234 <222> LOCATION: (27)..(1082)
236 <400> SEQUENCE: 3
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238                               Met Asp Tyr Gln Val Ser Ser Pro Ile
239                               1           5
241 tat gac atc aat tat tat aca tcg gag ccc tgc caa aaa atc aat gtg      101
242 Tyr Asp Ile Asn Tyr Tyr Thr Ser Glu Pro Cys Gln Lys Ile Asn Val
243 10                               15           20           25
245 aag caa atc gca gcc cgc ctc ctg cct ccg ctc tac tca ctg gtg ttc      149
246 Lys Gln Ile Ala Ala Arg Leu Leu Pro Pro Leu Tyr Ser Leu Val Phe
247                               30           35           40
249 atc ttt ggt ttt gtg ggc aac atg ctg gtc atc ctc atc ctg ata aac      197
250 Ile Phe Gly Phe Val Gly Asn Met Leu Val Ile Leu Ile Leu Ile Asn
251                               45           50           55
253 tgc aaa agg ctg aag agc atg act gac atc tac ctg ctc aac ctg gcc      245
254 Cys Lys Arg Leu Lys Ser Met Thr Asp Ile Tyr Leu Leu Asn Leu Ala
255                               60           65           70
257 atc tct gac ctg ttt ttc ctt act gtc ccc ttc tgg gct cac tat      293
258 Ile Ser Asp Leu Phe Phe Leu Leu Thr Val Pro Phe Trp Ala His Tyr
259                               75           80           85
261 gct gcc gcc cag tgg gac ttt gga aat aca atg tgt caa ctc ttg aca      341
262 Ala Ala Ala Gln Trp Asp Phe Gly Asn Thr Met Cys Gln Leu Leu Thr
263 90                               95           100          105
265 ggg ctc tat ttt ata ggc ttc ttc tct gga atc ttc ttc atc atc ctc      389
266 Gly Leu Tyr Phe Ile Gly Phe Phe Ser Gly Ile Phe Phe Ile Ile Leu
267                               110          115          120
269 ctg aca atc gat agg tac ctg gct gtc gtc cat gct gtg ttt gct tta      437
270 Leu Thr Ile Asp Arg Tyr Leu Ala Val Val His Ala Val Phe Ala Leu
271                               125          130          135
273 aaa gcc agg acg gtc acc ttt ggg gtg gtg aca agt gtg atc act tgg      485
274 Lys Ala Arg Thr Val Thr Phe Gly Val Val Thr Ser Val Ile Thr Trp
275                               140          145          150
277 gtg gtg gct gtg ttt gcg tct ctc cca gga atc atc ttt acc aga tct      533
278 Val Val Ala Val Phe Ala Ser Leu Pro Gly Ile Ile Phe Thr Arg Ser
279                               155          160          165
281 caa aaa gaa ggt ctt cat tac acc tgc agc tct cat ttt cca tac agt      581
282 Gln Lys Glu Gly Leu His Tyr Thr Cys Ser Ser His Phe Pro Tyr Ser
283 170                               175          180          185
285 cag tat caa ttc tgg aag aat ttc cag aca tta aag ata gtc atc ttg      629
286 Gln Tyr Gln Phe Trp Lys Asn Phe Gln Thr Leu Lys Ile Val Ile Leu
287                               190          195          200
289 ggg ctg gtc ctg ccg ctg ctt gtc atg gtc atc tgc tac tcg gga atc      677
290 Gly Leu Val Leu Pro Leu Leu Val Met Val Ile Cys Tyr Ser Gly Ile
291                               205          210          215

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293 cta aaa act ctg ctt cgg tgt cga aat gag aag aag agg cac agg gct      725
294 Leu Lys Thr Leu Leu Arg Cys Arg Asn Glu Lys Lys Arg His Arg Ala
295      220      225      230
297 gtg agg ctt atc ttc acc atc atg att gtt tat ttt ctc ttc tgg gct      773
298 Val Arg Leu Ile Phe Thr Ile Met Ile Val Tyr Phe Leu Phe Trp Ala
299      235      240      245
301 ccc tac aac att gtc ctt ctc ctg aac acc ttc cag gaa ttc ttt ggc      821
302 Pro Tyr Asn Ile Val Leu Leu Leu Asn Thr Phe Gln Glu Phe Phe Gly
303 250      255      260      265
305 ctg aat aat tgc agt agc tct aac agg ttg gac caa gct atg cag gtg      869
306 Leu Asn Asn Cys Ser Ser Ser Asn Arg Leu Asp Gln Ala Met Gln Val
307      270      275      280
309 aca gag act ctt ggg atg acg cac tgc tgc atc aac ccc atc atc tat      917
310 Thr Glu Thr Leu Gly Met Thr His Cys Cys Ile Asn Pro Ile Ile Tyr
311      285      290      295
313 gcc ttt gtc ggg gag aag ttc aga aac tac ctc tta gtc ttc ttc caa      965
314 Ala Phe Val Gly Glu Lys Phe Arg Asn Tyr Leu Leu Val Phe Phe Gln
315      300      305      310
317 aag cac att gcc aaa cgc ttc tgc aaa tgc tgt tct att ttc cag caa      1013
318 Lys His Ile Ala Lys Arg Phe Cys Lys Cys Cys Ser Ile Phe Gln Gln
319      315      320      325
321 gag gct ccc gag cga gca agc tca gtt tac acc cga tcc act ggg gag      1061
322 Glu Ala Pro Glu Arg Ala Ser Ser Val Tyr Thr Arg Ser Thr Gly Glu
323 330      335      340      345
325 cag gaa ata tct gtg ggc ttg tgacacggac tcaagtgggc tggtgaccca      1112
326 Gln Glu Ile Ser Val Gly Leu
327      350
329 gtcagagttg tgcacatggc ttagtttttca tacacagcct gggctggggg tggggtggga      1172
331 gaggtctttt ttaaaaggaa gttactgtta tagagggtct aagattcatc cat      1225
334 <210> SEQ ID NO: 4
335 <211> LENGTH: 352
336 <212> TYPE: PRT
337 <213> ORGANISM: Homo sapiens
339 <400> SEQUENCE: 4
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345 Ser Glu Pro Cys Gln Lys Ile Asn Val Lys Gln Ile Ala Ala Arg Leu
346      20      25      30
349 Leu Pro Pro Leu Tyr Ser Leu Val Phe Ile Phe Gly Phe Val Gly Asn
350      35      40      45
353 Met Leu Val Ile Leu Ile Leu Ile Asn Cys Lys Arg Leu Lys Ser Met
354      50      55      60
357 Thr Asp Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp Leu Phe Phe Leu
358 65      70      75      80
361 Leu Thr Val Pro Phe Trp Ala His Tyr Ala Ala Ala Gln Trp Asp Phe
362      85      90      95
365 Gly Asn Thr Met Cys Gln Leu Leu Thr Gly Leu Tyr Phe Ile Gly Phe
366      100      105      110
369 Phe Ser Gly Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu

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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 03/21/2006
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; Xaa Pos. 1

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:10

VERIFICATION SUMMARY

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Input Set : A:\seq listing.app

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L:442 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0